

SEQUENCE LISTING

substitute

(1) GENERAL INFORMATION: --

- (i) APPLICANT: Ill, Charles R. et al.
- (ii) TITLE OF INVENTION: NOVEL VECTORS AND GENES EXHIBITING INCREASED EXPRESSION
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
 - (B) STREET: 28 STATE STREET
 - (C) CITY: BOSTON
 - (D) STATE: MASSACHUSETTS
 - (E) COUNTRY: US
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 04 DECEMBER 1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA: /
 - (A) APPLICATION NUMBER: US 60/067,614
 - (B) FILING DATE: 05 DECEMBER 1997
 - (A) APPLICATION NUMBER: US 60/071,596
 - (B) FILING DATE: 16 JANUARY 1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: REMILLARD, JANE E.
 - (B) REGISTRATION NUMBER: 38,872
 - (C) REFERENCE/DOCKET NUMBER: TTI-180
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)742-4214

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..4374

[illegible]

2

AAA AGT TGG CAC TCA GAA ACA AAG AAC TCC CTC ATG CAA GAT AGG GAT	720
Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp	
225 230 235 240	
GCT GCA TCT GCT CGG GCC TGG CCT AAA ATG CAC ACA GTC AAT GGT TAT	768
Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr	
245 250 255	
GTA AAC AGG AGC CTG CCA GGA CTG ATT GGA TGC CAC AGG AAA TCA GTC	816
Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val	
260 265 270	
TAT TGG CAT GTT ATA GGA ATG GGC ACC ACT CCT GAA GTG CAC TCA ATA	864
Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile	
275 280 285	
TTC CTC GAA GGA CAC ACA TTT CTT GTT AGA AAC CAT CGC CAG GCG TCC	912
Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser	
290 295 300	
TTG GAA ATC TCG CCA ATA ACT TTC CTT ACT GCT CAA ACA CTC CTC ATG	960
Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met	
305 310 315 320	
GAC CTT GGA CAG TTT CTA CTG TTT TGT CAT ATC TCT TCC CAC CAA CAT	1008
Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His	
325 330 335	
GAT GGC ATG GAA GCT TAT GTC AAA GTA GAC AGC TGT CCA GAG GAA CCC	1056
Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro	
340 345 350	
CAA CTA CGA ATG AAA AAT AAT GAA GAA GCG GAA GAC TAT GAT GAT GAT	1104
Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp	
355 360 365	
CTT ACC GAT TCT GAA ATG GAT GTG GTC AGA TTT GAT GAT GAC AAC TCT	1152
Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser	
370 375 380	
CCT TCC TTT ATC CAA ATT CGC TCA GTT GCC AAG AAG CAT CCT AAA ACT	1200
Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr	
385 390 395 400	
TGG GTA CAT TAC ATT GCT GCT GAA GAG GAG GAC TGG GAC TAT GCT CCC	1248
Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro	
405 410 415	
TTA GTC CTC GCC CCC GAT GAC AGA AGT TAT AAA AGT CAA TAT TTG AAC	1296
Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn	
420 425 430	
AAT GGC CCT CAG CGG ATT GGA AGG AAG TAC AAA AAA GTC CGA TTT ATG	1344
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met	
435 440 445	

GCA TAC ACA GAT GAA ACC TTT AAG ACT CGT GAA GCT ATT CAG CAT GAA	1392
Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu	
450 455 460	
TCA GGA ATC TTG GGA CCT TTA CTT TAT GGG GAA GTT GGA GAC ACA CTG	1440
Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu	
465 470 475 480	
CTC ATT ATA TTT AAG AAT CAA GCA AGC AGA CCA TAT AAC ATC TAC CCT	1488
Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro	
485 490 495	
CAC GGA ATC ACC GAT GTC CGT CCT TTG TAT TCA CGC AGA TTA CCA AAA	1536
His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys	
500 505 510	
GGA GTA AAA CAT TTG AAG GAT TTT CCA ATT CTG CCC GGA GAA ATA TTC	1584
Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe	
515 520 525	
AAA TAT AAA TGG ACA GTG ACT GTA GAA GAT GGG CCA ACT AAA TCA GAT	1632
Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp	
530 535 540	
CCT CGG TGC CTG ACC CGC TAT TAC TCT AGT TTC GTC AAT ATG GAG AGA	1680
Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg	
545 550 555 560	
GAT CTA GCT TCA GGA CTC ATT GGC CCT CTC CTC ATC TGC TAC AAA GAA	1728
Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu	
565 570 575	
TCT GTA GAT CAA AGA GGA AAC CAG ATA ATG TCA GAC AAG AGG AAT GTC	1776
Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val	
580 585 590	
ATC CTG TTT TCT GTA TTT GAT GAG AAC CGA AGC TGG TAC CTC ACA GAG	1824
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu	
595 600 605	
AAT ATA CAA CGC TTT CTC CCC AAT CCC GCT GGA GTG CAG CTT GAG GAT	1872
Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp	
610 615 620	
CCA GAG TTC CAA GCC TCC AAC ATC ATG CAC AGC ATC AAT GGC TAT GTT	1920
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val	
625 630 635 640	
TTC GAT AGT TTG CAG TTG TCA GTT TGT TTG CAT GAA GTA GCA TAC TGG	1968
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp	
645 650 655	
TAC ATT CTA AGC ATT GGA GCA CAG ACT GAC TTC CTT TCT GTC TTC TTC	2016
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe	
660 665 670	

TCT GGA TAT ACC TTC AAA CAC AAA ATG GTC TAT GAA GAC ACA CTC ACC	2064
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr	
675 680 685	
CTA TTC CCA TTC TCC GGA GAA ACT GTC TTC ATG TCG ATG GAA AAC CCA	2112
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro	
690 695 700	
GGA CTA TGG ATT CTG GGG TGC CAC AAC TCA GAC TTT CGG AAC AGA GGC	2160
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly	
705 710 715 720	
ATG ACC GCC TTA CTG AAA GTT TCC AGT TGT GAC AAG AAC ACT GGA GAT	2208
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp	
725 730 735	
TAT TAC GAG GAC AGT TAT GAA GAT ATT TCA GCA TAC TTG CTG AGT AAA	2256
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Ser Lys	
740 745 750	
AAC AAT GCC ATT GAA CCA AGA AGC TTC TCC CAG AAC CCA CCA GTC TTG	2304
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu	
755 760 765	
AAA CGC CAT CAA CGG GAA ATA ACT CGT ACT ACT CTT CAA TCA GAT CAA	2352
Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln	
770 775 780	
GAG GAA ATT GAC TAT GAT GAT ACC ATA TCA GTT GAA ATG AAG AAG GAA	2400
Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu	
785 790 795 800	
GAT TTC GAC ATT TAT GAT GAG GAT GAA AAT CAG AGC CCC CGC AGC TTT	2448
Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe	
805 810 815	
CAA AAG AAA ACA CGA CAC TAT TTT ATT GCT GCA GTG GAG AGG CTC TGG	2496
Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp	
820 825 830	
GAT TAT GGG ATG AGT AGC TCC CCA CAT GTT CTA AGA AAC AGG GCT CAG	2544
Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln	
835 840 845	
AGT GGC AGT GTC CCT CAG TTC AAG AAA GTA GTA TTC CAG GAA TTT ACC	2592
Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr	
850 855 860	
GAT GGC TCC TTT ACT CAA CCC TTA TAC CGT GGA GAA CTA AAT GAA CAT	2640
Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His	
865 870 875 880	
TTG GGA CTC CTG GGG CCA TAT ATA AGA GCA GAA GTT GAA GAT AAT ATC	2688
Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile	
885 890 895	

ATG	GTT	ACC	TTC	AGA	AAT	CAG	GCC	TCT	CGT	CCC	TAT	TCC	TTC	TAT	TCT	2736
Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	
			900					905					910			
TCC	CTC	ATA	TCA	TAT	GAG	GAA	GAT	CAG	AGG	CAA	GGA	GCA	GAA	CCT	AGA	2784
Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	
		915					920					925				
AAA	AAC	TTT	GTC	AAG	CCT	AAT	GAA	ACC	AAA	ACT	TAC	TTT	TGG	AAA	GTG	2832
Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	
	930					935					940					
CAA	CAT	CAT	ATG	GCA	CCC	ACT	AAA	GAT	GAG	TTT	GAC	TGC	AAA	GCC	TGG	2880
Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	
945					950					955					960	
GCT	TAT	TTC	TCC	GAT	GTC	GAC	CTG	GAA	AAA	GAT	GTG	CAC	TCA	GGC	CTG	2928
Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	
			965					970						975		
ATT	GGA	CCC	CTT	CTG	GTC	TGC	CAC	ACC	AAC	ACA	CTG	AAC	CCT	GCT	CAT	2976
Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	
		980						985					990			
GGG	AGA	CAA	GTG	ACA	GTA	CAG	GAA	TTT	GCT	CTG	TTT	TTC	ACC	ATC	TTC	3024
Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	
		995					1000					1005				
GAT	GAG	ACC	AAA	AGC	TGG	TAC	TTC	ACT	GAA	AAT	ATG	GAA	AGA	AAC	TGC	3072
Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	
	1010					1015					1020					
AGG	GCT	CCC	TGC	AAT	ATC	CAG	ATG	GAA	GAT	CCC	ACT	TTT	AAA	GAG	AAT	3120
Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys	Glu	Asn	
1025					1030					1035					1040	
TAT	CGC	TTC	CAT	GCA	ATC	AAT	GGC	TAC	ATA	ATG	GAT	ACA	CTA	CCT	GGC	3168
Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr	Leu	Pro	Gly	
			1045					1050						1055		
TTA	GTA	ATG	GCT	CAG	GAT	CAA	AGG	ATT	CGA	TGG	TAT	CTG	CTC	AGC	ATG	3216
Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp	Tyr	Leu	Leu	Ser	Met	
			1060					1065					1070			
GGC	AGC	AAT	GAA	AAC	ATC	CAT	TCT	ATT	CAT	TTC	TCC	GGA	CAT	GTG	TTC	3264
Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe	Ser	Gly	His	Val	Phe	
		1075					1080					1085				
ACT	GTA	CGA	AAA	AAA	GAG	GAG	TAT	AAA	ATG	GCA	CTG	TAC	AAT	CTC	TAT	3312
Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	Ala	Leu	Tyr	Asn	Leu	Tyr	
	1090					1095					1100					
CCC	GGA	GTT	TTC													

TGG	CGG	GTG	GAA	TGC	CTT	ATT	GGC	GAG	CAT	CTA	CAT	GCT	GGG	ATG	AGC	3408
Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His	Leu	His	Ala	Gly	Met	Ser	
				1125					1130					1135		
ACA	CTT	TTT	CTG	GTG	TAC	TCC	AAT	AAG	TGT	CAG	ACT	CCC	CTG	GGA	ATG	3456
Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Met	
			1140					1145					1150			
GCT	TCT	GGA	CAC	ATT	AGA	GAT	TTT	CAG	ATT	ACA	GCT	TCA	GGA	CAA	TAT	3504
Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	Thr	Ala	Ser	Gly	Gln	Tyr	
		1155					1160					1165				
GGA	CAG	TGG	GCC	CCA	AAG	CTG	GCC	AGA	CTT	CAT	TAT	TCC	GGA	TCA	ATC	3552
Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu	His	Tyr	Ser	Gly	Ser	Ile	
	1170					1175				1180						
AAT	GCC	TGG	AGC	ACC	AAG	GAG	CCC	TTT	TCT	TGG	ATC	AAA	GTT	GAC	CTG	3600
Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser	Trp	Ile	Lys	Val	Asp	Leu	
1185				1190					1195						1200	
TTG	GCA	CCA	ATG	ATT	ATT	CAC	GGC	ATC	AAG	ACC	CAG	GGT	GCC	CGT	CAG	3648
Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	
			1205					1210					1215			
AAG	TTC	TCC	AGC	CTC	TAC	ATC	TCT	CAA	TTT	ATC	ATC	ATG	TAT	AGT	CTC	3696
Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	
		1220				1225						1230				
GAT	GGG	AAG	AAG	TGG	CAG	ACT	TAT	CGA	GGA	AAT	TCC	ACT	GGA	ACC	CTC	3744
Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	
	1235					1240					1245					
ATG	GTC	TTC	TTT	GGC	AAT	GTG	GAT	TCA	TCT	GGG	ATA	AAA	CAC	AAT	ATT	3792
Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	
	1250				1255					1260						
TTC	AAC	CCT	CCA	ATT	ATT	GCT	CGA	TAC	ATC	CGT	TTG	CAC	CCA	ACT	CAT	3840
Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	
1265				1270					1275						1280	
TAT	AGC	ATT	CGC	AGC	ACT	CTT	CGC	ATG	GAG	TTG	ATG	GGC	TGT	GAT	TTA	3888
Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	
			1285					1290					1295			
AAT	AGT	TGC	AGC	ATG	CCA	TTG	GGA	ATG	GAG	AGT	AAA	GCA	ATA	TCA	GAT	3936
Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	
		1300				1305						1310				
GCA	CAG	ATT	ACT	GCT	TCA	TCC	TAC	TTT	ACC	AAT	ATG	TTT	GCC	ACC	TGG	3984
Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	Trp	
	1315					1320					1325					

AGA CCT CAA GTT AAC AAT CCA AAA GAG TGG CTG CAA GTG GAC TTC CAG	4080
Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln	
1345 1350 1355 1360	
AAG ACA ATG AAA GTC ACA GGA GTA ACT ACT CAG GGA GTA AAA TCT CTG	4128
Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu	
1365 1370 1375	
CTT ACC TCT ATG TAC GTG AAG GAG TTC CTC ATA TCG TCG TCG CAA GAT	4176
Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp	
1380 1385 1390	
GGC CAT CAG TGG ACT CTC TTT TTT CAA AAT GGC AAA GTA AAA GTT TTC	4224
Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe	
1395 1400 1405	
CAG GGA AAT CAA GAC TCC TTC ACA CCT GTC GTG AAC TCT CTA GAC CCA	4272
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro	
1410 1415 1420	
CCG TTA CTC ACT CGC TAC CTT CGA ATT CAC CCC CAG AGT TGG GTG CAC	4320
Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His	
1425 1430 1435 1440	
CAG ATT GCC CTG AGG ATG GAG GTT CTG GGC TGC GAG GCA CAG GAC CTC	4368
Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu	
1445 1450 1455	
TAC TGA	4374
Tyr	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1006..5376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTCGACGGTA TCGATAAGCT TGATATCGAA TTCCTGCAGC CCGGGGGATC CACTAGTACT	60
CGAGACCTAG GAGTTAATTT TTAAAAAGCA GTCAAAAGTC CAAGTGGCCC TTGCGAGCAT	120
TTACTCTCTC TGTTTGCTCT GGTTAATAAT CTCAGGAGCA CAAACATTCC TTACTAGTCC	180
TAGAAGTTAA TTTTAAAAA GCAGTCAAAA GTCCAAGTGG CCCTTGCGAG CATTTACTCT	240
CTCTGTTTGC TCTGGTTAAT AATCTCAGGA GCACAAACAT TCCTTACTAG TTCTAGAGCG	300
GCCGCCAGTG TGCTGGAATT CGGCTTTTTT AGGGCTGGAA GCTACCTTTG ACATCATTTT	360

CTCTGCGAAT	GCATGTATAA	TTTCTACAGA	ACCTATTAGA	AAGGATCACC	CAGCCTCTGC		420
TTTTGTACAA	CTTTCCCTTA	AAAAACTGCC	AATTCCTACTG	CTGTTTGGCC	CAATAGTGAG		480
AACTTTTTTCC	TGCTGCCTCT	TGGTGCTTTT	GCCTATGGCC	CCTATTCTGC	CTGCTGAAGA		540
CACTCTTGCC	AGCATGGACT	TAAACCCCTC	CAGCTCTGAC	AATCCTCTTT	CTCTTTTGTT		600
TTACATGAAG	GGTCTGGCAG	CCAAAGCAAT	CACTCAAAGT	TCAAACCTTA	TCATTTTTTG		660
CTTTGTTCTT	CTTGGCCTTG	GTTTTGTACA	TCAGCTTTGA	AAATACCATC	CCAGGGTTAA		720
TGCTGGGGTT	AATTTATAAC	TAAGAGTGCT	CTAGTTTTGC	AATACAGGAC	ATGCTATAAA		780
AATGGAAAGA	TGTTGCTTTC	TGAGAGATCT	CGAGGAAGCT	AACAACAAAG	AACAACAAAC		840
AACAATCAGG	TAAGTATCCT	TTTACAGCA	CAACTTAATG	AGACAGATAG	AAACTGGTCT		900
TGTAGAAACA	GAGTAGTCGC	CTGCTTTTCT	GCCAGGTGCT	GACTTCTCTC	CCCTTCTCTT		960
TTTTCCTTTT	CTCAGGATAA	CAAGAACGAA	ACAATAACAG	CCACC	ATG GAA ATA		1014
					Met Glu Ile		
					1		
GAG CTC TCC ACC TGC TTC TTT CTG TGC CTT TTG CGA TTC TGC TTT AGT							1062
Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser							
5						10	
							15
GCC ACC AGA AGA TAC TAC CTG GGT GCA GTG GAA CTG TCA TGG GAC TAT							1110
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr							
20					25		30
							35
ATG CAA AGT GAT CTC GGT GAG CTG CCT GTG GAC GCA AGA TTT CCT CCT							1158
Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro							
			40				45
							50
AGA GTG CCA AAA TCT TTT CCA TTC AAC ACC TCA GTC GTG TAC AAA AAG							1206
Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys							
		55					60
							65
ACT CTG TTT GTA GAA TTC ACG GTT CAC CTT TTC AAC ATC GCT AAG CCA							1254
Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile Ala Lys Pro							
		70					75
							80
AGG CCA CCC TGG ATG GGT CTG CTA GGT CCT ACC ATC CAG GCT GAG GTT							1302
Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val							
		85					90
							95
TAT GAT ACA GTG GTC ATT ACA CTT AAG AAC ATG GCT TCC CAT CCT GTC							1350
Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val							
100					105		110
							115
AGT CTT CAT GCT GTT GGT GTA TCC TAC TGG AAA GCT TCT GAG GGA GCT							1398
Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala							
			120				125
							130

GAA TAT GAT GAT CAG ACC AGT CAA AGG GAG AAA GAA GAT GAT AAA GTC	1446
Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val	
135 140 145	
TTC CCT GGT GGA AGC CAT ACA TAT GTC TGG CAG GTC CTG AAA GAG AAT	1494
Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn	
150 155 160	
GGT CCA ATG GCC TCT GAC CCA CTG TGC CTT ACC TAC TCA TAT CTT TCT	1542
Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser	
165 170 175	
CAT GTG GAC CTG GTA AAA GAC TTG AAT TCA GGC CTC ATT GGA GCC CTA	1590
His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu	
180 185 190 195	
CTA GTA TGT AGA GAA GGG AGT CTG GCC AAG GAA AAG ACA CAG ACC TTG	1638
Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu	
200 205 210	
CAC AAA TTT ATA CTA CTT TTT GCT GTA TTT GAT GAA GGG AAA AGT TGG	1686
His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp	
215 220 225	
CAC TCA GAA ACA AAG AAC TCC TTG ATG CAG GAT AGG GAT GCT GCA TCT	1734
His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser	
230 235 240	
GCT CGG GCC TGG CCT AAA ATG CAC ACA GTC AAT GGT TAT GTA AAC AGG	1782
Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg	
245 250 255	
TCT CTG CCA GGT CTG ATT GGA TGC CAC AGG AAA TCA GTC TAT TGG CAT	1830
Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His	
260 265 270 275	
GTG ATT GGA ATG GGC ACC ACT CCT GAA GTG CAC TCA ATA TTC CTC GAA	1878
Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu	
280 285 290	
GGT CAC ACA TTT CTT GTG AGG AAC CAT CGC CAG GCG TCC TTG GAA ATC	1926
Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile	
295 300 305	
TCG CCA ATA ACT TTC CTT ACT GCT CAA ACA CTC TTG ATG GAC CTT GGA	1974
Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly	
310 315 320	
CAG TTT CTA CTG TTT TGT CAT ATC TCT TCC CAC CAA CAT GAT GGC ATG	2022
Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met	
325 330 335	
GAA GCT TAT GTC AAA GTA GAC AGC TGT CCA GAG GAA CCC CAA CTA CGA	2070
Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg	
340 345 350 355	

ATG AAA AAT AAT GAA GAA GCG GAA GAC TAT GAT GAT GAT CTT ACT GAT	2118
Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp	
360 365 370	
TCT GAA ATG GAT GTG GTC AGG TTT GAT GAT GAC AAC TCT CCT TCC TTT	2166
Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe	
375 380 385	
ATC CAA ATT CGC TCA GTT GCC AAG AAG CAT CCT AAA ACT TGG GTA CAT	2214
Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His	
390 395 400	
TAC ATT GCT GCT GAA GAG GAG GAC TGG GAC TAT GCT CCC TTA GTC CTC	2262
Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu	
405 410 415	
GCC CCC GAT GAC AGA AGT TAT AAA AGT CAA TAT TTG AAC AAT GGC CCT	2310
Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro	
420 425 430 435	
CAG CGG ATT GGT AGG AAG TAC AAA AAA GTC CGA TTT ATG GCA TAC ACA	2358
Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr	
440 445 450	
GAT GAA ACC TTT AAG ACT CGT GAA GCT ATT CAG CAT GAA TCA GGA ATC	2406
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile	
455 460 465	
TTG GGA CCT TTA CTT TAT GGG GAA GTT GGA GAC ACA CTG TTG ATT ATA	2454
Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile	
470 475 480	
TTT AAG AAT CAA GCA AGC AGA CCA TAT AAC ATC TAC CCT CAC GGA ATC	2502
Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile	
485 490 495	
ACT GAT GTC CGT CCT TTG TAT TCA AGG AGA TTA CCA AAA GGT GTA AAA	2550
Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys	
500 505 510 515	
CAT TTG AAG GAT TTT CCA ATT CTG CCA GGA GAA ATA TTC AAA TAT AAA	2598
His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys	
520 525 530	
TGG ACA GTG ACT GTA GAA GAT GGG CCA ACT AAA TCA GAT CCT CGG TGC	2646
Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys	
535 540 545	
CTG ACC CGC TAT TAC TCT AGT TTC GTT AAT ATG GAG AGA GAT CTA GCT	2694
Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala	
550 555 560	
TCA GGA CTC ATT GGC CCT CTC CTC ATC TGC TAC AAA GAA TCT GTA GAT	2742
Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp	
565 570 575	

CAA AGA GGA AAC CAG ATA ATG TCA GAC AAG AGG AAT GTC ATC CTG TTT	2790
Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe	
580 585 590 595	
TCT GTA TTT GAT GAG AAC CGA AGC TGG TAC CTC ACA GAG AAT ATA CAA	2838
Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln	
600 605 610	
CGC TTT CTC CCC AAT CCA GCT GGA GTG CAG CTT GAG GAT CCA GAG TTC	2886
Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe	
615 620 625	
CAA GCC TCC AAC ATC ATG CAC AGC ATC AAT GGC TAT GTT TTT GAT AGT	2934
Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser	
630 635 640	
TTG CAG TTG TCA GTT TGT TTG CAT GAG GTG GCA TAC TGG TAC ATT CTA	2982
Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu	
645 650 655	
AGC ATT GGA GCA CAG ACT GAC TTC CTT TCT GTC TTC TTC TCT GGA TAT	3030
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr	
660 665 670 675	
ACC TTC AAA CAC AAA ATG GTC TAT GAA GAC ACA CTC ACC CTA TTC CCA	3078
Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro	
680 685 690	
TTC TCA GGA GAA ACT GTC TTC ATG TCG ATG GAA AAC CCA GGT CTA TGG	3126
Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp	
695 700 705	
ATT CTG GGG TGC CAC AAC TCA GAC TTT CGG AAC AGA GGC ATG ACC GCC	3174
Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala	
710 715 720	
TTA CTG AAG GTT TCT AGT TGT GAC AAG AAC ACT GGT GAT TAT TAC GAG	3222
Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu	
725 730 735	
GAC AGT TAT GAA GAT ATT TCA GCA TAC TTG CTG AGT AAA AAC AAT GCC	3270
Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala	
740 745 750 755	
ATT GAA CCA AGA AGC TTC TCC CAG AAC CCA CCA GTC TTG AAA CGC CAT	3318
Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu Lys Arg His	
760 765 770	
CAA CGG GAA ATA ACT CGT ACT ACT CTT CAG TCA GAT CAA GAG GAA ATT	3366
Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile	
775 780 785	
GAC TAT GAT GAT ACC ATA TCA GTT GAA ATG AAG AAG GAA GAT TTT GAC	3414
Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp	
790 795 800	

ATT TAT GAT GAG GAT GAA AAT CAG AGC CCC CGC AGC TTT CAA AAG AAA	3462
Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys	
805 810 815	
ACA CGA CAC TAT TTT ATT GCT GCA GTG GAG AGG CTC TGG GAT TAT GGG	3510
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly	
820 825 830 835	
ATG AGT AGC TCC CCA CAT GTT CTA AGA AAC AGG GCT CAG AGT GGC AGT	3558
Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser	
840 845 850	
GTC CCT CAG TTC AAG AAA GTT GTT TTC CAG GAA TTT ACT GAT GGC TCC	3606
Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser	
855 860 865	
TTT ACT CAG CCC TTA TAC CGT GGA GAA CTA AAT GAA CAT TTG GGA CTC	3654
Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu	
870 875 880	
CTG GGG CCA TAT ATA AGA GCA GAA GTT GAA GAT AAT ATC ATG GTA ACT	3702
Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr	
885 890 895	
TTC AGA AAT CAG GCC TCT CGT CCC TAT TCC TTC TAT TCT AGC CTT ATT	3750
Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile	
900 905 910 915	
TCT TAT GAG GAA GAT CAG AGG CAA GGA GCA GAA CCT AGA AAA AAC TTT	3798
Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe	
920 925 930	
GTC AAG CCT AAT GAA ACC AAA ACT TAC TTT TGG AAA GTG CAA CAT CAT	3846
Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His	
935 940 945	
ATG GCA CCC ACT AAA GAT GAG TTT GAC TGC AAA GCC TGG GCT TAT TTC	3894
Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe	
950 955 960	
TCT GAT GTT GAC CTG GAA AAA GAT GTG CAC TCA GGC CTG ATT GGA CCC	3942
Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro	
965 970 975	
CTT CTG GTC TGC CAC ACT AAC ACA CTG AAC CCT GCT CAT GGG AGA CAA	3990
Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln	
980 985 990 995	
GTG ACA GTA CAG GAA TTT GCT CTG TTT TTC ACC ATC TTT GAT GAG ACC	4038
Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr	
1000 1005 1010	
AAA AGC TGG TAC TTC ACT GAA AAT ATG GAA AGA AAC TGC AGG GCT CCC	4086
Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro	
1015 1020 1025	

TGC AAT ATC CAG ATG GAA GAT CCC ACT TTT AAA GAG AAT TAT CGC TTC Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe 1030 1035 1040	4134
CAT GCA ATC AAT GGC TAC ATA ATG GAT ACA CTA CCT GGC TTA GTA ATG His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met 1045 1050 1055	4182
GCT CAG GAT CAA AGG ATT CGA TGG TAT CTG CTC AGC ATG GGC AGC AAT Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn 1060 1065 1070 1075	4230
GAA AAC ATC CAT TCT ATT CAT TTC AGT GGA CAT GTG TTC ACT GTA CGA Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg 1080 1085 1090	4278
AAA AAA GAG GAG TAT AAA ATG GCA CTG TAC AAT CTC TAT CCA GGT GTT Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val 1095 1100 1105	4326
TTT GAG ACA GTG GAA ATG TTA CCA TCC AAA GCT GGA ATT TGG CGG GTG Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val 1110 1115 1120	4374
GAA TGC CTT ATT GGC GAG CAT CTA CAT GCT GGG ATG AGC ACA CTT TTT Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe 1125 1130 1135	4422
CTG GTG TAC AGC AAT AAG TGT CAG ACT CCC CTG GGA ATG GCT TCT GGA Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly 1140 1145 1150 1155	4470
CAC ATT AGA GAT TTT CAG ATT ACA GCT TCA GGA CAA TAT GGA CAG TGG His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp 1160 1165 1170	4518
GCC CCA AAG CTG GCC AGA CTT CAT TAT TCC GGA TCA ATC AAT GCC TGG Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp 1175 1180 1185	4566
AGC ACC AAG GAG CCC TTT TCT TGG ATC AAG GTG GAT CTG TTG GCA CCA Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro 1190 1195 1200	4614
ATG ATT ATT CAC GGC ATC AAG ACC CAG GGT GCC CGT CAG AAG TTC TCC Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser 1205 1210 1215	4662
AGC CTC TAC ATC TCT CAG TTT ATC ATC ATG TAT AGT CTT GAT GGG AAG Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys 1220 1225 1230 1235	4710
AAG TGG CAG ACT TAT CGA GGA AAT TCC ACT GGA ACC TTA ATG GTC TTC Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe 1240 1245 1250	4758

TTT GGC AAT GTG GAT TCA TCT GGG ATA AAA CAC AAT ATT TTT AAC CCT	4806
Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro	
1255 1260 1265	
CCA ATT ATT GCT CGA TAC ATC CGT TTG CAC CCA ACT CAT TAT AGC ATT	4854
Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile	
1270 1275 1280	
CGC AGC ACT CTT CGC ATG GAG TTG ATG GGC TGT GAT TTA AAT AGT TGC	4902
Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys	
1285 1290 1295	
AGC ATG CCA TTG GGA ATG GAG AGT AAA GCA ATA TCA GAT GCA CAG ATT	4950
Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile	
1300 1305 1310 1315	
ACT GCT TCA TCC TAC TTT ACC AAT ATG TTT GCC ACC TGG TCT CCT TCA	4998
Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser	
1320 1325 1330	
AAA GCT CGA CTT CAC CTC CAA GGG AGG AGT AAT GCC TGG AGA CCT CAG	5046
Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln	
1335 1340 1345	
GTG AAT AAT CCA AAA GAG TGG CTG CAA GTG GAC TTC CAG AAG ACA ATG	5094
Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met	
1350 1355 1360	
AAA GTC ACA GGA GTA ACT ACT CAG GGA GTA AAA TCT CTG CTT ACC AGC	5142
Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser	
1365 1370 1375	
ATG TAT GTG AAG GAG TTC CTC ATC TCC AGC AGT CAA GAT GGC CAT CAG	5190
Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln	
1380 1385 1390 1395	
TGG ACT CTC TTT TTT CAG AAT GGC AAA GTA AAG GTT TTT CAG GGA AAT	5238
Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn	
1400 1405 1410	
CAA GAC TCC TTC ACA CCT GTG GTG AAC TCT CTA GAC CCA CCG TTA CTG	5286
Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu	
1415 1420 1425	
ACT CGC TAC CTT CGA ATT CAC CCC CAG AGT TGG GTG CAC CAG ATT GCC	5334
Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala	
1430 1435 1440	
CTG AGG ATG GAG GTT CTG GGC TGC GAG GCA CAG GAC CTC TAC	5376
Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr	
1445 1450 1455	
TGAGGGTGGC CACTGCAGCA CCTGCCACTG CCGTCACCTC TCCCTCCTCA GCTCCAGGGC	5436
AGTGTCCCTC CCTGGCTTGC CTTCTACCTT TGTGCTAAAT CCTAGCAGAC ACTGCCTTGA	5496
AGCCTCCTGA ATTAACATC ATCAGTCCTG CATTTCTTTG GTGGGGGGCC AGGAGGGTGC	5556

ATCCAATTTA	ACTTAACTCT	TACCTATTTT	CTGCAGCTGC	TCCAGATTA	CTCCTTCCTT	5616
CCAATATAAC	TAGGCAAAAA	GAAGTGAGGA	GAAACCTGCA	TGAAAGCATT	CTTCCCTGAA	5676
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TGAAAAAGAT	ATTTATGATG	TTAACTTGTT	TATTGCAGCT	TATAATGGTT	ACAAATAAAG	5796
CAATAGCATC	ACAAATTTCA	CAAATAAAGC	ATTTTTTTCA	CTGCATTCTA	GTTGTGGTTT	5856
GTCCAAACTC	ATCAATGTAT	CTTATCATGT	CTGGATCCCC	GGGTGGCATC	CCTGTGACCC	5916
CTCCCCAGTG	CCTCTCCTGG	CCCTGGAAGT	TGCCACTCCA	GTGCCCACCA	GCCTTGTCTT	5976
AATAAAATTA	AGTTGCATCA	TTTTGTCTGA	CTAGGTGTCC	TTCTATAATA	TTATGGGGTG	6036
GAGGGGGGTG	GTATGGAGCA	AGGGGCAAGT	TGGGAAGACA	ACCTGTAGGG	CCTGCGGGGT	6096
CTATTCGGGA	ACCAAGCTGG	AGTGCAGTGG	CACAATCTTG	GCTCACTGCA	ATCTCCGCCT	6156
CCTGGGTTCA	AGCGATTCTC	CTGCCTCAGC	CTCCCGAGTT	GTTGGGATTC	CAGGCATGCA	6216
TGACCAGGCT	CAGCTAATTT	TTGTTTTTTT	GGTAGAGACG	GGGTTTCACC	ATATTGGCCA	6276
GGCTGGTCTC	CAACTCCTAA	TCTCAGGTGA	TCTACCCACC	TTGGCCTCCC	AAATTGCTGG	6336
GATTACAGGC	GTGAACCACT	GCTCCCTTCC	CTGTCCTTCT	GATTTTAAAA	TAACTATAACC	6396
AGCAGGAGGA	CGTCCAGACA	CAGCATAGGC	TACCTGCCAT	GCCCAACCGG	TGGGACATTT	6456
GAGTTGCTTG	CTTGGCACTG	TCCTCTCATG	CGTTGGGTCC	ACTCAGTAGA	TGCCTGTTGA	6516
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ACAACATACG	AGCCGGAAGC	ATAAAGTGTA	AAGCCTGGGG	TGCCTAATGA	GTGAGCTAAC	6636
TCACATTAAT	TGCGTTGCGC	TCACTGCCCG	CTTTCCAGTC	GGGAAACCTG	TCGTGCCAGC	6696
TGCATTAATG	AATCGGCCAA	CGCGCGGGGA	GAGGCGGTTT	GCGTATTGGG	CGCTCTTCCG	6756
CTTCCTCGCT	CACTGACTCG	CTGCGCTCGG	TCGTTCGGCT	GCGGCGAGCG	GTATCAGCTC	6816
ACTCAAAGGC	GGTAATACGG	TTATCCACAG	AATCAGGGGA	TAACGCAGGA	AAGAACATGT	6876
GAGCAAAAGG	CCAGCAAAAG	GCCAGGAACC	GTAAAAAGGC	CGCGTTGCTG	GCGTTTTTCC	6936
ATAGGCTCCG	CCCCCCTGAC	GAGCATCACA	AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	6996
ACCCGACAGG	ACTATAAAGA	TACCAGGCGT	TTCCCCCTGG	AAGCTCCCTC	GTGCGCTCTC	7056
CTGTTCCGAC	CCTGCCGCTT	ACCGGATACC	TGTCCGCCTT	TCTCCCTTCG	GGAAGCGTGG	7116
CGCTTTCTCA	TAGCTCACGC	TGTAGGTATC	TCAGTTCGGT	GTAGGTCGTT	CGCTCCAAGC	7176
TGGGCTGTGT	GCACGAACCC	CCCGTTCAGC	CCGACCGCTG	CGCCTTATCC	GGTAACTATC	7236
GTCTTGAGTC	CAACCCGGTA	AGACACGACT	TATCGCCACT	GGCAGCAGCC	ACTGGTAACA	7296

GGATTAGCAG	AGCGAGGTAT	GTAGGCGGTG	CTACAGAGTT	CTTGAAGTGG	TGGCCTAACT	7356
ACGGCTACAC	TAGAAGGACA	GTATTTGGTA	TCTGCGCTCT	GCTGAAGCCA	GTTACCTTCG	7416
GAAAAAGAGT	TGGTAGCTCT	TGATCCGGCA	AACAAACCAC	CGCTGGTAGC	GGTGGTTTTT	7476
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GATTATCAAA	AAGGATCTTC	ACCTAGATCC	TTTTAAATTA	AAAATGAAGT	TTAAATCAA	7656
TCTAAAGTAT	ATATGAGTAA	ACTTGGTCTG	ACAGTTACCA	ATGCTTAATC	AGTGAGGCAC	7716
CTATCTCAGC	GATCTGTCTA	TTTCGTTTCT	CCATAGTTGC	CTGACTCCCC	GTCGTGTAGA	7776
TAACCTACGAT	ACGGGAGGGC	TTACCATCTG	GCCCCAGTGC	TGCAATGATA	CCGCGAGACC	7836
CACGCTCACC	GGCTCCAGAT	TTATCAGCAA	TAAACCAGCC	AGCCGGAAGG	GCCGAGCGCA	7896
GAAGTGGTCC	TGCAACTTTA	TCCGCCTCCA	TCCAGTCTAT	TAATTGTTGC	CGGGAAGCTA	7956
GAGTAAGTAG	TTCGCCAGTT	AATAGTTTGC	GCAACGTTGT	TGCCATTGCT	ACAGGCATCG	8016
TGGTGTACAG	CTCGTCGTTT	GGTATGGCTT	CATTCAGCTC	CGGTTCCCAA	CGATCAAGGC	8076
GAGTTACATG	ATCCCCCATG	TTGTGCAAAA	AAGCGGTTAG	CTCCTTCGGT	CCTCCGATCG	8136
TTGTCAGAAG	TAAGTTGGCC	GCAGTGTTAT	CACTCATGGT	TATGGCAGCA	CTGCATAATT	8196
CTCTTACTGT	CATGCCATCC	GTAAGATGCT	TTTCTGTGAC	TGGTGAGTAC	TCAACCAAGT	8256
CATTCTGAGA	ATAGTGTATG	CGGCGACCGA	GTTGCTCTTG	CCCGGCGTCA	ATACGGGATA	8316
ATACCGCGCC	ACATAGCAGA	ACTTTAAAAG	TGCTCATCAT	TGGAAAACGT	TCTTCGGGGC	8376
GAAAACTCTC	AAGGATCTTA	CCGCTGTTGA	GATCCAGTTC	GATGTAACCC	ACTCGTGCAC	8436
CCAACTGATC	TTCAGCATCT	TTTACTTTCA	CCAGCGTTTC	TGGGTGAGCA	AAAACAGGAA	8496
GGCAAAATGC	CGCAAAAAG	GGAATAAGGG	CGACACGGAA	ATGTTGAATA	CTCATACTCT	8556
TCCTTTTTTCA	ATATTATTGA	AGCATTTATC	AGGGTTATTG	TCTCATGAGC	GGATACATAT	8616
TTGAATGTAT	TTAGAAAAAT	AAACAAATAG	GGGTTCCGCG	CACATTTCCC	CGAAAAGTGC	8676
CACCTGACGT	CTAAGAAACC	ATTATTATCA	TGACATTAAC	CTATAAAAAT	AGGCGTATCA	8736
CGAGGCCCTT	TCGTCTCGCG	CGTTTCGGTG	ATGACGGTGA	AAACCTCTGA	CACATGCAGC	8796
TCCCGGAGAC	GGTCACAGCT	TGTCTGTAAG	CGGATGCCGG	GAGCAGACAA	GCCCGTCAGG	8856
GCGCGTCAGC	GGGTGTTGGC	GGGTGTCGGG	GCTGGCTTAA	CTATGCGGCA	TCAGAGCAGA	8916
TTGTACTGAG	AGTGCACCAT	ATGCGGTGTG	AAATACCGCA	CAGATGCGTA	AGGAGAAAAT	8976
ACCGCATCAG	GCGCCATTTC	CCATTCAGGC	TGCGCAACTG	TTGGGAAGGG	CGATCGGTGC	9036

GGGCTCTTC	GCTATTACGC	CAGCTGGCGA	AAGGGGGATG	TGCTGCAAGG	CGATTAAGTT	9096
GGGTAACGCC	AGGGTTTTTC	CAGTCACGAC	GTTGTAAAC	GACGGCCAGT	GCCAAGCTTG	9156
GGCTGCAG						9164

(2) INFORMATION FOR SEQ ID NO:3:

(ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS
(B) LOCATION: 1006..3294

(A) NAME/KEY: CDS
(B) LOCATION: 6153..8234

GTCCAGCGGTA	TCGATAAGCT	TGATATCGAA	TTCCTGCAGC	CCGGGGGATC	CACTAGTACT	60
CGAGACCTAG	GAGTTAATTT	TAAAAAAGCA	GTCAAAAGTC	CAAGTGGCCC	TTGCGAGCAT	120
TTACTCTCTC	TGTTTGCTCT	GGTTAATAAT	CTCAGGAGCA	CAAACATTCC	TTACTAGTCC	180
TAGAAGTTAA	TTTTTAAAAA	GCAGTCAAAA	GTCCAAGTGG	CCCTTGCGAG	CATTTACTCT	240
CTCTGTTTGC	TCTGGTTAAT	AATCTCAGGA	GCACAAACAT	TCCTTACTAG	TTCTAGAGCG	300
GCCGCCAGTG	TGCTGGAATT	CGGCTTTTTT	AGGGCTGGAA	GCTACCTTTG	ACATCATTTT	360
CTCTGCGAAT	GCATGTATAA	TTTCTACAGA	ACCTATTAGA	AAGGATCACC	CAGCCTCTGC	420
TTTTGTACAA	CTTTCCCTTA	AAAAACTGCC	AATTCCACTG	CTGTTTGGCC	CAATAGTGAG	480
AACTTTTTTC	TGCTGCCTCT	TGGTGCTTTT	GCCTATGGCC	CCTATTCTGC	CTGCTGAAGA	540
CACTCTTGCC	AGCATGGACT	TAAACCCCTC	CAGCTCTGAC	AATCCTCTTT	CTCTTTTGTT	600
TTACATGAAG	GGTCTGGCAG	CCAAAGCAAT	CACTCAAAGT	TCAAACCTTA	TCATTTTTTG	660
CTTTGTTCCCT	CTTGGCCTTG	GTTTTGTACA	TCAGCTTTGA	AAATACCATC	CCAGGGTTAA	720
TGCTGGGGTT	AATTTATAAC	TAAGAGTGCT	CTAGTTTTGC	AATACAGGAC	ATGCTATAAA	780
AATGGAAAGA	TGTTGCTTTC	TGAGAGATCT	CGAGGAAGCT	AACAACAAAG	AACAACAAAC	840
AACAATCAGG	TAAGTATCCT	TTTTACAGCA	CAACTTAATG	AGACAGATAG	AAACTGGTCT	900
TGTAGAAACA	GAGTAGTCGC	CTGCTTTTCT	GCCAGGTGCT	GACTTCTCTC	CCCTTCTCTT	960

TTTTCTTTT CTCAGGATAA CAAGAACGAA ACAATAACAG CCACC ATG GAA ATA	1014
Met Glu Ile	
1	
GAG CTC TCC ACC TGC TTC TTT CTG TGC CTT TTG CGA TTC TGC TTT AGT	1062
Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser	
5 10 15	
GCC ACC AGA AGA TAC TAC CTG GGT GCA GTG GAA CTG TCA TGG GAC TAT	1110
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr	
20 25 30 35	
ATG CAA AGT GAT CTC GGT GAG CTG CCT GTG GAC GCA AGA TTT CCT CCT	1158
Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro	
40 45 50	
AGA GTG CCA AAA TCT TTT CCA TTC AAC ACC TCA GTC GTG TAC AAA AAG	1206
Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys	
55 60 65	
ACT CTG TTT GTA GAA TTC ACG GTT CAC CTT TTC AAC ATC GCT AAG CCA	1254
Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile Ala Lys Pro	
70 75 80	
AGG CCA CCC TGG ATG GGT CTG CTA GGT CCT ACC ATC CAG GCT GAG GTT	1302
Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val	
85 90 95	
TAT GAT ACA GTG GTC ATT ACA CTT AAG AAC ATG GCT TCC CAT CCT GTC	1350
Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val	
100 105 110 115	
AGT CTT CAT GCT GTT GGT GTA TCC TAC TGG AAA GCT TCT GAG GGA GCT	1398
Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala	
120 125 130	
GAA TAT GAT GAT CAG ACC AGT CAA AGG GAG AAA GAA GAT GAT AAA GTC	1446
Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val	
135 140 145	
TTC CCT GGT GGA AGC CAT ACA TAT GTC TGG CAG GTC CTG AAA GAG AAT	1494
Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn	
150 155 160	
GGT CCA ATG GCC TCT GAC CCA CTG TGC CTT ACC TAC TCA TAT CTT TCT	1542
Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser	
165 170 175	
CAT GTG GAC CTG GTA AAA GAC TTG AAT TCA GGC CTC ATT GGA GCC CTA	1590
His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu	
180 185 190 195	
CTA GTA TGT AGA GAA GGG AGT CTG GCC AAG GAA AAG ACA CAG ACC TTG	1638
Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu	
200 205 210	

CAC AAA TTT ATA CTA CTT TTT GCT GTA TTT GAT GAA GGG AAA AGT TGG	1686
His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp	
215 220 225	
CAC TCA GAA ACA AAG AAC TCC TTG ATG CAG GAT AGG GAT GCT GCA TCT	1734
His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser	
230 235 240	
GCT CGG GCC TGG CCT AAA ATG CAC ACA GTC AAT GGT TAT GTA AAC AGG	1782
Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg	
245 250 255	
TCT CTG CCA GGT CTG ATT GGA TGC CAC AGG AAA TCA GTC TAT TGG CAT	1830
Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His	
260 265 270 275	
GTG ATT GGA ATG GGC ACC ACT CCT GAA GTG CAC TCA ATA TTC CTC GAA	1878
Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu	
280 285 290	
GGT CAC ACA TTT CTT GTG AGG AAC CAT CGC CAG GCG TCC TTG GAA ATC	1926
Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile	
295 300 305	
TCG CCA ATA ACT TTC CTT ACT GCT CAA ACA CTC TTG ATG GAC CTT GGA	1974
Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly	
310 315 320	
CAG TTT CTA CTG TTT TGT CAT ATC TCT TCC CAC CAA CAT GAT GGC ATG	2022
Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met	
325 330 335	
GAA GCT TAT GTC AAA GTA GAC AGC TGT CCA GAG GAA CCC CAA CTA CGA	2070
Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg	
340 345 350 355	
ATG AAA AAT AAT GAA GAA GCG GAA GAC TAT GAT GAT GAT CTT ACT GAT	2118
Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp	
360 365 370	
TCT GAA ATG GAT GTG GTC AGG TTT GAT GAT GAC AAC TCT CCT TCC TTT	2166
Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe	
375 380 385	
ATC CAA ATT CGC TCA GTT GCC AAG AAG CAT CCT AAA ACT TGG GTA CAT	2214
Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His	
390 395 400	
TAC ATT GCT GCT GAA GAG GAG GAC TGG GAC TAT GCT CCC TTA GTC CTC	2262
Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu	
405 410 415	
GCC CCC GAT GAC AGA AGT TAT AAA AGT CAA TAT TTG AAC AAT GGC CCT	2310
Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro	
420 425 430 435	

CAG CGG ATT GGT AGG AAG TAC AAA AAA GTC CGA TTT ATG GCA TAC ACA	2358
Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr	
440 445 450	
GAT GAA ACC TTT AAG ACT CGT GAA GCT ATT CAG CAT GAA TCA GGA ATC	2406
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile	
455 460 465	
TTG GGA CCT TTA CTT TAT GGG GAA GTT GGA GAC ACA CTG TTG ATT ATA	2454
Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile	
470 475 480	
TTT AAG AAT CAA GCA AGC AGA CCA TAT AAC ATC TAC CCT CAC GGA ATC	2502
Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile	
485 490 495	
ACT GAT GTC CGT CCT TTG TAT TCA AGG AGA TTA CCA AAA GGT GTA AAA	2550
Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys	
500 505 510 515	
CAT TTG AAG GAT TTT CCA ATT CTG CCA GGA GAA ATA TTC AAA TAT AAA	2598
His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys	
520 525 530	
TGG ACA GTG ACT GTA GAA GAT GGG CCA ACT AAA TCA GAT CCT CGG TGC	2646
Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys	
535 540 545	
CTG ACC CGC TAT TAC TCT AGT TTC GTT AAT ATG GAG AGA GAT CTA GCT	2694
Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala	
550 555 560	
TCA GGA CTC ATT GGC CCT CTC CTC ATC TGC TAC AAA GAA TCT GTA GAT	2742
Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp	
565 570 575	
CAA AGA GGA AAC CAG ATA ATG TCA GAC AAG AGG AAT GTC ATC CTG TTT	2790
Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe	
580 585 590 595	
TCT GTA TTT GAT GAG AAC CGA AGC TGG TAC CTC ACA GAG AAT ATA CAA	2838
Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln	
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CGC TTT CTC CCC AAT CCA GCT GGA GTG CAG CTT GAG GAT CCA GAG TTC	2886
Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe	
615 620 625	
CAA GCC TCC AAC ATC ATG CAC AGC ATC AAT GGC TAT GTT TTT GAT AGT	2934
Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser	
630 635 640	
TTG CAG TTG TCA GTT TGT TTG CAT GAG GTG GCA TAC TGG TAC ATT CTA	2982
Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu	
645 650 655	

AGC ATT GGA GCA CAG ACT GAC TTC CTT TCT GTC TTC TTC TCT GGA TAT	3030
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr	
660 665 670 675	
ACC TTC AAA CAC AAA ATG GTC TAT GAA GAC ACA CTC ACC CTA TTC CCA	3078
Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro	
680 685 690	
TTC TCA GGA GAA ACT GTC TTC ATG TCG ATG GAA AAC CCA GGT CTA TGG	3126
Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp	
695 700 705	
ATT CTG GGG TGC CAC AAC TCA GAC TTT CGG AAC AGA GGC ATG ACC GCC	3174
Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala	
710 715 720	
TTA CTG AAG GTT TCT AGT TGT GAC AAG AAC ACT GGT GAT TAT TAC GAG	3222
Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu	
725 730 735	
GAC AGT TAT GAA GAT ATT TCA GCA TAC TTG CTG AGT AAA AAC AAT GCC	3270
Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala	
740 745 750 755	
ATT GAA CCA AGA AGC TTC TCC CAG GTAAGTTATT ATATAAATTC AAGACACCCT	3324
Ile Glu Pro Arg Ser Phe Ser Gln	
760	
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GAGGCATTTT TACCCACTTG GTACATAAAA TTATTGGGTC ACCCTTTTCC TCTTCTTTTT 6144

TTCTCCAG AAC CCA CCA GTC TTG AAA CGC CAT CAA CGG GAA ATA ACT CGT 6194
 Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
 1 5 10

ACT ACT CTT CAG TCA GAT CAA GAG GAA ATT GAC TAT GAT GAT ACC ATA 6242
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile
 15 20 25 30

TCA GTT GAA ATG AAG AAG GAA GAT TTT GAC ATT TAT GAT GAG GAT GAA 6290
 Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu
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AAT CAG AGC CCC CGC AGC TTT CAA AAG AAA ACA CGA CAC TAT TTT ATT 6338
 Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile
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GCT GCA GTG GAG AGG CTC TGG GAT TAT GGG ATG AGT AGC TCC CCA CAT 6386
 Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His
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GTT CTA AGA AAC AGG GCT CAG AGT GGC AGT GTC CCT CAG TTC AAG AAA 6434
 Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys
 80 85 90

GTT GTT TTC CAG GAA TTT ACT GAT GGC TCC TTT ACT CAG CCC TTA TAC 6482
 Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr
 95 100 105 110

CGT GGA GAA CTA AAT GAA CAT TTG GGA CTC CTG GGG CCA TAT ATA AGA 6530
 Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
 115 120 125

GCA GAA GTT GAA GAT AAT ATC ATG GTA ACT TTC AGA AAT CAG GCC TCT 6578
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser
 130 135 140

CGT CCC TAT TCC TTC TAT TCT AGC CTT ATT TCT TAT GAG GAA GAT CAG 6626
 Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln
 145 150 155

AGG CAA GGA GCA GAA CCT AGA AAA AAC TTT GTC AAG CCT AAT GAA ACC 6674
 Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr
 160 165 170

AAA ACT TAC TTT TGG AAA GTG CAA CAT CAT ATG GCA CCC ACT AAA GAT 6722
 Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp
 175 180 185 190

GAG TTT GAC TGC AAA GCC TGG GCT TAT TTC TCT GAT GTT GAC CTG GAA 6770
 Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu
 195 200 205

AAA GAT GTG CAC TCA GGC CTG ATT GGA CCC CTT CTG GTC TGC CAC ACT	6818
Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr	
210 215 220	
AAC ACA CTG AAC CCT GCT CAT GGG AGA CAA GTG ACA GTA CAG GAA TTT	6866
Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe	
225 230 235	
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Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr	
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Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu	
255 260 265 270	
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Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr	
275 280 285	
ATA ATG GAT ACA CTA CCT GGC TTA GTA ATG GCT CAG GAT CAA AGG ATT	7058
Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile	
290 295 300	
CGA TGG TAT CTG CTC AGC ATG GGC AGC AAT GAA AAC ATC CAT TCT ATT	7106
Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile	
305 310 315	
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His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys	
320 325 330	
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Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met	
335 340 345 350	
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Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu	
355 360 365	
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Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln	
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Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg	
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Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe	
415 420 425 430	

TCT TGG ATC AAG GTG GAT CTG TTG GCA CCA ATG ATT ATT CAC GGC ATC	7490
Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile	
435 440 445	
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Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln	
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Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg	
465 470 475	
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Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser	
480 485 490	
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Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr	
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Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met	
515 520 525	
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Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met	
530 535 540	
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Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe	
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Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu	
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Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu	
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TGG CTG CAA GTG GAC TTC CAG AAG ACA ATG AAA GTC ACA GGA GTA ACT	7970
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr	
595 600 605	
ACT CAG GGA GTA AAA TCT CTG CTT ACC AGC ATG TAT GTG AAG GAG TTC	8018
Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe	
610 615 620	
CTC ATC TCC AGC AGT CAA GAT GGC CAT CAG TGG ACT CTC TTT TTT CAG	8066
Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln	
625 630 635	
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Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro	
640 645 650	

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Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile	
655 660 665 670	
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His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu	
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Gly Cys Glu Ala Gln Asp Leu Tyr	
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AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAGGCGT	9884
TTCCCCCTGG	AAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	CCTGCCGCTT	ACCGGATACC	9944
TGTCCGCCTT	TCTCCCTTCG	GGAAGCGTGG	CGCTTTCTCA	TAGCTCACGC	TGTAGGTATC	10004
TCAGTTCGGT	GTAGGTCGTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	CCCGTTCAGC	10064
CCGACCGCTG	CGCCTTATCC	GGTAACTATC	GTCTTGAGTC	CAACCCGGTA	AGACACGACT	10124
TATCGCCACT	GGCAGCAGCC	ACTGGTAACA	GGATTAGCAG	AGCGAGGTAT	GTAGGCGGTG	10184
CTACAGAGTT	CTTGAAGTGG	TGGCCTAACT	ACGGCTACAC	TAGAAGGACA	GTATTTGGTA	10244
TCTGCGCTCT	GCTGAAGCCA	GTTACCTTCG	GAAAAAGAGT	TGGTAGCTCT	TGATCCGGCA	10304
AACAAACCAC	CGCTGGTAGC	GGTGGTTTTT	TTGTTTGCAA	GCAGCAGATT	ACGCGCAGAA	10364
AAAAAGGATC	TCAAGAAGAT	CCTTTGATCT	TTTCTACGGG	GTCTGACGCT	CAGTGGAACG	10424
AAAACTCACG	TTAAGGGATT	TTGGTCATGA	GATTATCAAA	AAGGATCTTC	ACCTAGATCC	10484
TTTTAAATTA	AAAATGAAGT	TTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	ACTTGGTCTG	10544
ACAGTTACCA	ATGCTTAATC	AGTGAGGCAC	CTATCTCAGC	GATCTGTCTA	TTTCGTTTCAT	10604
CCATAGTTGC	CTGACTCCCC	GTCGTGTAGA	TAACTACGAT	ACGGGAGGGC	TTACCATCTG	10664
GCCCCAGTGC	TGCAATGATA	CCGCGAGACC	CACGCTCACC	GGCTCCAGAT	TTATCAGCAA	10724
TAAACCAGCC	AGCCGGAAGG	GCCGAGCGCA	GAAGTGGTCC	TGCAACTTTA	TCCGCCTCCA	10784
TCCAGTCTAT	TAATTGTTGC	CGGGAAGCTA	GAGTAAGTAG	TTCGCCAGTT	AATAGTTTGC	10844
GCAACGTTGT	TGCCATTGCT	ACAGGCATCG	TGGTGTCACG	CTCGTCGTTT	GGTATGGCTT	10904
CATTCAGCTC	CGGTTCCCAA	CGATCAAGGC	GAGTTACATG	ATCCCCCATG	TTGTGCAAAA	10964
AAGCGGTTAG	CTCCTTCGGT	CCTCCGATCG	TTGTCAGAAAG	TAAGTTGGCC	GCAGTGTTAT	11024
CACTCATGGT	TATGGCAGCA	CTGCATAATT	CTCTTACTGT	CATGCCATCC	GTAAGATGCT	11084
TTTCTGTGAC	TGGTGAGTAC	TCAACCAAGT	CATTCTGAGA	ATAGTGTATG	CGGCGACCGA	11144
GTTGCTCTTG	CCCGGCGTCA	ATACGGGATA	ATACCGCGCC	ACATAGCAGA	ACTTTAAAAG	11204
TGCTCATCAT	TGGAAAACGT	TCTTCGGGGC	GAAAACTCTC	AAGGATCTTA	CCGCTGTTGA	11264
GATCCAGTTC	GATGTAACCC	ACTCGTGCAC	CCAACTGATC	TTCAGCATCT	TTTACTTTCA	11324
CCAGCGTTTT	TGGGTGAGCA	AAAACAGGAA	GGCAAAATGC	CGCAAAAAAG	GGAATAAGGG	11384

CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTCA ATATTATTGA AGCATTTATC 11444
 AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG 11504
 GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT CTAAGAAACC ATTATTATCA 11564
 TGACATTAAC CTATAAAAAT AGGCGTATCA CGAGGCCCTT TCGTCTCGCG CGTTTCGGTG 11624
 ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC GGTCACAGCT TGTCTGTAAG 11684
 CGGATGCCGG GAGCAGACAA GCCCGTCAGG GCGCGTCAGC GGGTGTGGC GGGTGTGGG 11744
 GCTGGCTTAA CTATGCGGCA TCAGAGCAGA TTGTACTGAG AGTGCACCAT ATGCGGTGTG 11804
 AAATACCGCA CAGATGCGTA AGGAGAAAAT ACCGCATCAG GCGCCATTCG CCATTCAGGC 11864
 TGCGCAACTG TTGGGAAGGG CGATCGGTGC GGGCCTCTTC GCTATTACGC CAGCTGGCGA 11924
 AAGGGGGATG TGCTGCAAGG CGATTAAGTT GGGTAACGCC AGGGTTTTCC CAGTCACGAC 11984
 GTTGTA AAC GACGGCCAGT GCCAAGCTTG GGCTGCAG 12022

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1006..8058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGACGGTA TCGATAAGCT TGATATCGAA TTCCTGCAGC CCGGGGGATC CACTAGTACT 60
 CGAGACCTAG GAGTTAATTT TTAAAAAGCA GTCAAAAGTC CAAGTGGCCC TTGCGAGCAT 120
 TTA CTCTCTC TGTTTGCTCT GGTAAATAAT CTCAGGAGCA CAAACATTCC TTA CTAGTCC 180
 TAGAAGTTAA TTTTAAAAA GCAGTCAAAA GTCCAAGTGG CCCTTGCGAG CATTTACTCT 240
 CTCTGTTTGC TCTGGTTAAT AATCTCAGGA GCACAAACAT TCCTTACTAG TTCTAGAGCG 300
 GCCGCCAGTG TGCTGGAATT CGGCTTTTTT AGGGCTGGAA GCTACCTTTG ACATCATTTT 360
 CTCTGCGAAT GCATGTATAA TTTCTACAGA ACCTATTAGA AAGGATCACC CAGCCTCTGC 420
 TTTTGTACAA CTTTCCCTTA AAAAAGTACC AATTCCACTG CTGTTTGGCC CAATAGTGAG 480
 AACTTTTTTC TGCTGCCTCT TGGTGCTTTT GCCTATGGCC CCTATTCTGC CTGCTGAAGA 540
 CACTCTTGCC AGCATGGACT TAAACCCCTC CAGCTCTGAC AATCCTCTTT CTCTTTTGTT 600

TTACATGAAG GGTCTGGCAG CCAAAGCAAT CACTCAAAGT TCAAACCTTA TCATTTTTTTG	660
CTTTGTTTCCT CTTGGCCTTG GTTTTGTACA TCAGCTTTGA AAATACCATC CCAGGGTTAA	720
TGCTGGGGTT AATTTATAAC TAAGAGTGCT CTAGTTTTGC AATACAGGAC ATGCTATAAA	780
AATGGAAAGA TGTTGCTTTC TGAGAGATCT CGAGGAAGCT AACAACAAAG AACAACAAAC	840
AACAATCAGG TAAGTATCCT TTTTACAGCA CAACTTAATG AGACAGATAG AAACCTGGTCT	900
TGTAGAAACA GAGTAGTCGC CTGCTTTTCT GCCAGGTGCT GACTTCTCTC CCCTTCTCTT	960
TTTTCCTTTT CTCAGGATAA CAAGAACGAA ACAATAACAG CCACC ATG GAA ATA	1014
Met Glu Ile	
1	
GAG CTC TCC ACC TGC TTC TTT CTG TGC CTT TTG CGA TTC TGC TTT AGT	1062
Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser	
5 10 15	
GCC ACC AGA AGA TAC TAC CTG GGT GCA GTG GAA CTG TCA TGG GAC TAT	1110
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr	
20 25 30 35	
ATG CAA AGT GAT CTC GGT GAG CTG CCT GTG GAC GCA AGA TTT CCT CCT	1158
Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro	
40 45 50	
AGA GTG CCA AAA TCT TTT CCA TTC AAC ACC TCA GTC GTG TAC AAA AAG	1206
Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys	
55 60 65	
ACT CTG TTT GTA GAA TTC ACG GTT CAC CTT TTC AAC ATC GCT AAG CCA	1254
Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile Ala Lys Pro	
70 75 80	
AGG CCA CCC TGG ATG GGT CTG CTA GGT CCT ACC ATC CAG GCT GAG GTT	1302
Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val	
85 90 95	
TAT GAT ACA GTG GTC ATT ACA CTT AAG AAC ATG GCT TCC CAT CCT GTC	1350
Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val	
100 105 110 115	
AGT CTT CAT GCT GTT GGT GTA TCC TAC TGG AAA GCT TCT GAG GGA GCT	1398
Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala	
120 125 130	
GAA TAT GAT GAT CAG ACC AGT CAA AGG GAG AAA GAA GAT GAT AAA GTC	1446
Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val	
135 140 145	
TTC CCT GGT GGA AGC CAT ACA TAT GTC TGG CAG GTC CTG AAA GAG AAT	1494
Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn	
150 155 160	

GGT CCA ATG GCC TCT GAC CCA CTG TGC CTT ACC TAC TCA TAT CTT TCT	1542
Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser	
165 170 175	
CAT GTG GAC CTG GTA AAA GAC TTG AAT TCA GGC CTC ATT GGA GCC CTA	1590
His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu	
180 185 190 195	
CTA GTA TGT AGA GAA GGG AGT CTG GCC AAG GAA AAG ACA CAG ACC TTG	1638
Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu	
200 205 210	
CAC AAA TTT ATA CTA CTT TTT GCT GTA TTT GAT GAA GGG AAA AGT TGG	1686
His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp	
215 220 225	
CAC TCA GAA ACA AAG AAC TCC TTG ATG CAG GAT AGG GAT GCT GCA TCT	1734
His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser	
230 235 240	
GCT CGG GCC TGG CCT AAA ATG CAC ACA GTC AAT GGT TAT GTA AAC AGG	1782
Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg	
245 250 255	
TCT CTG CCA GGT CTG ATT GGA TGC CAC AGG AAA TCA GTC TAT TGG CAT	1830
Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His	
260 265 270 275	
GTG ATT GGA ATG GGC ACC ACT CCT GAA GTG CAC TCA ATA TTC CTC GAA	1878
Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu	
280 285 290	
GGT CAC ACA TTT CTT GTG AGG AAC CAT CGC CAG GCG TCC TTG GAA ATC	1926
Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile	
295 300 305	
TCG CCA ATA ACT TTC CTT ACT GCT CAA ACA CTC TTG ATG GAC CTT GGA	1974
Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly	
310 315 320	
CAG TTT CTA CTG TTT TGT CAT ATC TCT TCC CAC CAA CAT GAT GGC ATG	2022
Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met	
325 330 335	
GAA GCT TAT GTC AAA GTA GAC AGC TGT CCA GAG GAA CCC CAA CTA CGA	2070
Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg	
340 345 350 355	
ATG AAA AAT AAT GAA GAA GCG GAA GAC TAT GAT GAT GAT CTT ACT GAT	2118
Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp	
360 365 370	
TCT GAA ATG GAT GTG GTC AGG TTT GAT GAT GAC AAC TCT CCT TCC TTT	2166
Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe	
375 380 385	

ATC Ile	CAA Gln	ATT Ile	CGC Arg	TCA Ser	GTT Val	GCC Ala	AAG Lys	AAG Lys	CAT His	CCT Pro	AAA Lys	ACT Thr	TGG Trp	GTA Val	CAT His	2214
390						395			400							
TAC Tyr	ATT Ile	GCT Ala	GCT Ala	GAA Glu	GAG Glu	GAG Glu	GAC Asp	TGG Trp	GAC Asp	TAT Tyr	GCT Ala	CCC Pro	TTA Leu	GTC Val	CTC Leu	2262
405						410			415							
GCC Ala	CCC Pro	GAT Asp	GAC Asp	AGA Arg	AGT Ser	TAT Tyr	AAA Lys	AGT Ser	CAA Gln	TAT Tyr	TTG Leu	AAC Asn	AAT Asn	GGC Gly	CCT Pro	2310
420			425			430			435							
CAG Gln	CGG Arg	ATT Ile	GGT Gly	AGG Arg	AAG Lys	TAC Tyr	AAA Lys	AAA Lys	GTC Val	CGA Arg	TTT Phe	ATG Met	GCA Ala	TAC Tyr	ACA Thr	2358
			440						445			450				
GAT Asp	GAA Glu	ACC Thr	TTT Phe	AAG Lys	ACT Thr	CGT Arg	GAA Glu	GCT Ala	ATT Ile	CAG Gln	CAT His	GAA Glu	TCA Ser	GGA Gly	ATC Ile	2406
			455			460			465							
TTG Leu	GGA Gly	CCT Pro	TTA Leu	CTT Leu	TAT Tyr	GGG Gly	GAA Glu	GTT Val	GGA Gly	GAC Asp	ACA Thr	CTG Leu	TTG Leu	ATT Ile	ATA Ile	2454
			470			475			480							
TTT Phe	AAG Lys	AAT Asn	CAA Gln	GCA Ala	AGC Ser	AGA Arg	CCA Pro	TAT Tyr	AAC Asn	ATC Ile	TAC Tyr	CCT Pro	CAC His	GGA Gly	ATC Ile	2502
485						490			495							
ACT Thr	GAT Asp	GTC Val	CGT Arg	CCT Pro	TTG Leu	TAT Tyr	TCA Ser	AGG Arg	AGA Arg	TTA Leu	CCA Pro	AAA Lys	GGT Gly	GTA Val	AAA Lys	2550
500			505			510			515							
CAT His	TTG Leu	AAG Lys	GAT Asp	TTT Phe	CCA Pro	ATT Ile	CTG Leu	CCA Pro	GGA Gly	GAA Glu	ATA Ile	TTC Phe	AAA Lys	TAT Tyr	AAA Lys	2598
			520			525			530							
TGG Trp	ACA Thr	GTG Val	ACT Thr	GTA Val	GAA Glu	GAT Asp	GGG Gly	CCA Pro	ACT Thr	AAA Lys	TCA Ser	GAT Asp	CCT Pro	CGG Arg	TGC Cys	2646
			535			540			545							
CTG Leu	ACC Thr	CGC Arg	TAT Tyr	TAC Tyr	TCT Ser	AGT Ser	TTC Phe	GTT Val	AAT Asn	ATG Met	GAG Glu	AGA Arg	GAT Asp	CTA Leu	GCT Ala	2694
550						555			560							
TCA Ser	GGA Gly	CTC Leu	ATT Ile	GGC Gly	CCT Pro	CTC Leu	CTC Leu	ATC Ile	TGC Cys	TAC Tyr	AAA Lys	GAA Glu	TCT Ser	GTA Val	GAT Asp	2742
565			570			575			580							
CAA Gln	AGA Arg	GGA Gly	AAC Asn	CAG Gln	ATA Ile	ATG Met	TCA Ser	GAC Asp	AAG Lys	AGG Arg	AAT Asn	GTC Val	ATC Ile	CTG Leu	TTT Phe	2790
580			585			590			595							
TCT Ser	GTA Val	TTT Phe	GAT Asp	GAG Glu	AAC Asn	CGA Arg	AGC Ser	TGG Trp	TAC Tyr	CTC Leu	ACA Thr	GAG Glu	AAT Asn	ATA Ile	CAA Gln	2838
			600			605			610							

CGC TTT CTC CCC AAT CCA GCT GGA GTG CAG CTT GAG GAT CCA GAG TTC	2886
Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe	
615 620 625	
CAA GCC TCC AAC ATC ATG CAC AGC ATC AAT GGC TAT GTT TTT GAT AGT	2934
Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser	
630 635 640	
TTG CAG TTG TCA GTT TGT TTG CAT GAG GTG GCA TAC TGG TAC ATT CTA	2982
Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu	
645 650 655	
AGC ATT GGA GCA CAG ACT GAC TTC CTT TCT GTC TTC TTC TCT GGA TAT	3030
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr	
660 665 670 675	
ACC TTC AAA CAC AAA ATG GTC TAT GAA GAC ACA CTC ACC CTA TTC CCA	3078
Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro	
680 685 690	
TTC TCA GGA GAA ACT GTC TTC ATG TCG ATG GAA AAC CCA GGT CTA TGG	3126
Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp	
695 700 705	
ATT CTG GGG TGC CAC AAC TCA GAC TTT CGG AAC AGA GGC ATG ACC GCC	3174
Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala	
710 715 720	
TTA CTG AAG GTT TCT AGT TGT GAC AAG AAC ACT GGT GAT TAT TAC GAG	3222
Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu	
725 730 735	
GAC AGT TAT GAA GAT ATT TCA GCA TAC TTG CTG AGT AAA AAC AAT GCC	3270
Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala	
740 745 750 755	
ATT GAA CCA AGA AGC TTC TCC CAG AAT TCA AGA CAC CCT AGC ACT AGG	3318
Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg	
760 765 770	
CAA AAG CAA TTT AAT GCC ACC ACA ATT CCA GAA AAT GAC ATA GAG AAG	3366
Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys	
775 780 785	
ACT GAC CCT TGG TTT GCA CAC AGA ACA CCT ATG CCT AAA ATA CAA AAT	3414
Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn	
790 795 800	
GTC TCC TCT AGT GAT TTG TTG ATG CTC TTG CGA CAG AGT CCT ACT CCA	3462
Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser Pro Thr Pro	
805 810 815	
CAT GGG CTA TCC TTA TCT GAT CTC CAA GAA GCC AAA TAT GAG ACT TTT	3510
His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr Glu Thr Phe	
820 825 830 835	

TCT Ser	GAT Asp	GAT Asp	CCA Pro	TCA Ser 840	CCT Pro	GGA Gly	GCA Ala	ATA Ile	GAC Asp 845	AGT Ser	AAT Asn	AAC Asn	AGC Ser	CTG Leu 850	TCT Ser	3558
GAA Glu	ATG Met	ACA Thr	CAC His 855	TTC Phe	AGG Arg	CCA Pro	CAG Gln	CTC Leu 860	CAT His	CAC His	AGT Ser	GGG Gly	GAC Asp 865	ATG Met	GTA Val	3606
TTT Phe	ACC Thr	CCT Pro	GAG Glu 870	TCA Ser	GGC Gly	CTC Leu	CAA Gln 875	TTA Leu	AGA Arg	TTA Leu	AAT Asn	GAG Glu 880	AAA Lys	CTG Leu	GGG Gly	3654
ACA Thr	ACT Thr 885	GCA Ala	GCA Ala	ACA Thr	GAG Glu	TTG Leu 890	AAG Lys	AAA Lys	CTT Leu	GAT Asp	TTC Phe 895	AAA Lys	GTT Val	TCT Ser	AGT Ser	3702
ACA Thr 900	TCA Ser	AAT Asn	AAT Asn	CTG Leu	ATT Ile 905	TCA Ser	ACA Thr	ATT Ile	CCA Pro	TCA Ser 910	GAC Asp	AAT Asn	TTG Leu	GCA Ala 915	GCA Ala	3750
GGT Gly	ACT Thr	GAT Asp	AAT Asn 920	ACA Thr	AGT Ser	TCC Ser	TTA Leu	GGA Gly	CCC Pro 925	CCA Pro	AGT Ser	ATG Met	CCA Pro	GTT Val 930	CAT His	3798
TAT Tyr	GAT Asp	AGT Ser	CAA Gln 935	TTA Leu	GAT Asp	ACC Thr	ACT Thr	CTA Leu 940	TTT Phe	GGC Gly	AAA Lys	AAG Lys	TCA Ser 945	TCT Ser	CCC Pro	3846
CTT Leu	ACT Thr	GAG Glu 950	TCT Ser	GGT Gly	GGA Gly	CCT Pro	CTG Leu 955	AGC Ser	TTG Leu	AGT Ser	GAA Glu	GAA Glu 960	AAT Asn	AAT Asn	GAT Asp	3894
TCA Ser	AAG Lys 965	TTG Leu	TTA Leu	GAA Glu	TCA Ser	GGT Gly 970	TTA Leu	ATG Met	AAT Asn	AGC Ser	CAA Gln 975	GAA Glu	AGT Ser	TCA Ser	TGG Trp	3942
GGA Gly 980	AAA Lys	AAT Asn	GTA Val	TCG Ser	TCA Ser	ACA Thr 985	GAG Glu	AGT Ser	GGT Gly	AGG Arg 990	TTA Leu	TTT Phe	AAA Lys	GGG Gly 995	AAA Lys	3990
AGA Arg	GCT Ala	CAT His	GGA Gly 1000	CCT Pro	GCT Ala	TTG Leu	TTG Leu	ACT Thr	AAA Lys 1005	GAT Asp	AAT Asn	GCC Ala	TTA Leu	TTC Phe 1010	AAA Lys	4038
GTT Val	AGC Ser	ATC Ile	TCT Ser 1015	TTG Leu	TTA Leu	AAG Lys	ACA Thr	AAC Asn 1020	AAA Lys	ACT Thr	TCC Ser	AAT Asn	AAT Asn	TCA Ser 1025	GCA Ala	4086
ACT Thr	AAT Asn	AGA Arg 1030	AAG Lys	ACT Thr	CAC His	ATT Ile	GAT Asp 1035	GGC Gly	CCA Pro	TCA Ser	TTA Leu	TTA Leu 1040	ATT Ile	GAG Glu	AAT Asn	4134
AGT Ser	CCA Pro	TCA Ser	GTC Val	TGG Trp	CAA Gln	AAT Asn 1050	ATA Ile	TTA Leu	GAA Glu	AGT Ser	GAC Asp 1055	ACT Thr	GAG Glu	TTT Phe	AAA Lys	4182

AAA GTG ACA CCT TTG ATT CAT GAC AGA ATG CTT ATG GAC AAA AAT GCT	4230
Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp Lys Asn Ala	
1060 1065 1070 1075	
ACA GCT TTG AGG CTA AAT CAT ATG TCA AAT AAA ACT ACT TCA TCA AAA	4278
Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser Lys	
1080 1085 1090	
AAC ATG GAA ATG GTC CAA CAG AAA AAA GAG GGC CCC ATT CCA CCA GAT	4326
Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp	
1095 1100 1105	
GCA CAA AAT CCA GAT ATG TCG TTC TTT AAG ATG CTA TTC TTG CCA GAA	4374
Ala Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu	
1110 1115 1120	
TCA GCA AGG TGG ATA CAA AGG ACT CAT GGA AAG AAC TCT CTG AAC TCT	4422
Ser Ala Arg Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser	
1125 1130 1135	
GGG CAA GGC CCC AGT CCA AAG CAA TTA GTA TCC TTA GGA CCA GAA AAA	4470
Gly Gln Gly Pro Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys	
1140 1145 1150 1155	
TCT GTG GAA GGT CAG AAT TTC TTG TCT GAG AAA AAC AAA GTG GTA GTA	4518
Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val	
1160 1165 1170	
GGA AAG GGT GAA TTT ACA AAG GAC GTA GGA CTC AAA GAG ATG GTT TTT	4566
Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe	
1175 1180 1185	
CCA AGC AGC AGA AAC CTA TTT CTT ACT AAC TTG GAT AAT TTA CAT GAA	4614
Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu	
1190 1195 1200	
AAT AAT ACA CAC AAT CAA GAA AAA AAA ATT CAG GAA GAA ATA GAA AAG	4662
Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu Lys	
1205 1210 1215	
AAG GAA ACA TTA ATC CAA GAG AAT GTA GTT TTG CCT CAG ATA CAT ACA	4710
Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr	
1220 1225 1230 1235	
GTG ACT GGC ACT AAG AAT TTC ATG AAG AAC CTT TTC TTA CTG AGC ACT	4758
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr	
1240 1245 1250	
AGG CAA AAT GTA GAA GGT TCA TAT GAG GGG GCA TAT GCT CCA GTA CTT	4806
Arg Gln Asn Val Glu Gly Ser Tyr Glu Gly Ala Tyr Ala Pro Val Leu	
1255 1260 1265	
CAA GAT TTT AGG TCA TTA AAT GAT TCA ACA AAT AGA ACA AAG AAA CAC	4854
Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His	
1270 1275 1280	

ACA GCT CAT TTC TCA AAA AAA GGG GAG GAA GAA AAC TTG GAA GGC TTG	4902
Thr Ala His Phe Ser Lys Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu	
1285 1290 1295	
GGA AAT CAA ACC AAG CAA ATT GTA GAG AAA TAT GCA TGC ACC ACA AGG	4950
Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys Thr Thr Arg	
1300 1305 1310 1315	
ATA TCT CCT AAT ACA AGC CAG CAG AAT TTT GTC ACG CAA CGT AGT AAG	4998
Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln Arg Ser Lys	
1320 1325 1330	
AGA GCT TTG AAA CAA TTC AGA CTC CCA CTA GAA GAA ACA GAA CTT GAA	5046
Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr Glu Leu Glu	
1335 1340 1345	
AAA AGG ATA ATT GTG GAT GAC ACC TCA ACC CAG TGG TCC AAA AAC ATG	5094
Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn Met	
1350 1355 1360	
AAA CAT TTG ACC CCG AGC ACC CTC ACA CAG ATA GAC TAC AAT GAG AAG	5142
Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys	
1365 1370 1375	
GAG AAA GGG GCC ATT ACT CAG TCT CCC TTA TCA GAT TGC CTT ACG AGG	5190
Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg	
1380 1385 1390 1395	
AGT CAT AGC ATC CCT CAA GCA AAT AGA TCT CCA TTA CCC ATT GCA AAG	5238
Ser His Ser Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys	
1400 1405 1410	
GTA TCA TCA TTT CCA TCT ATT AGA CCT ATA TAT CTG ACC AGG GTC CTA	5286
Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu	
1415 1420 1425	
TTC CAA GAC AAC TCT TCT CAT CTT CCA GCA GCA TCT TAT AGA AAG AAA	5334
Phe Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys	
1430 1435 1440	
GAT TCT GGG GTC CAA GAA AGC AGT CAT TTC TTA CAA GGA GCC AAA AAA	5382
Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys Lys	
1445 1450 1455	
AAT AAC CTT TCT TTA GCC ATT CTA ACC TTG GAG ATG ACT GGT GAT CAA	5430
Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly Asp Gln	
1460 1465 1470 1475	
AGA GAG GTT GGC TCC CTG GGG ACA AGT GCC ACA AAT TCA GTC ACA TAC	5478
Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr Tyr	
1480 1485 1490	
AAG AAA GTT GAG AAC ACT GTT CTC CCG AAA CCA GAC TTG CCC AAA ACA	5526
Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr	
1495 1500 1505	

TCT GGC AAA GTT GAA TTG CTT CCA AAA GTT CAC ATT TAT CAG AAG GAC	5574
Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp	
1510 1515 1520	
CTA TTC CCT ACG GAA ACT AGC AAT GGG TCT CCT GGC CAT CTG GAT CTC	5622
Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu	
1525 1530 1535	
GTG GAA GGG AGC CTT CTT CAG GGA ACA GAG GGA GCG ATT AAG TGG AAT	5670
Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn	
1540 1545 1550 1555	
GAA GCA AAC AGA CCT GGA AAA GTT CCC TTT CTG AGA GTA GCA ACA GAA	5718
Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg Val Ala Thr Glu	
1560 1565 1570	
AGC TCT GCA AAG ACT CCC TCC AAG CTA TTG GAT CCT CTT GCT TGG GAT	5766
Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp Pro Leu Ala Trp Asp	
1575 1580 1585	
AAC CAC TAT GGT ACT CAG ATA CCA AAA GAA GAG TGG AAA TCC CAA GAG	5814
Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu	
1590 1595 1600	
AAG TCA CCA GAA AAA ACA GCT TTT AAG AAA AAG GAT ACC ATT TTG TCC	5862
Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser	
1605 1610 1615	
CTG AAC GCT TGT GAA AGC AAT CAT GCA ATA GCA GCA ATA AAT GAG GGA	5910
Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly	
1620 1625 1630 1635	
CAA AAT AAG CCC GAA ATA GAA GTC ACC TGG GCA AAG CAA GGT AGG ACT	5958
Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr	
1640 1645 1650	
GAA AGG CTG TGC TCT CAA AAC CCA CCA GTC TTG AAA CGC CAT CAA CGG	6006
Glu Arg Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg	
1655 1660 1665	
GAA ATA ACT CGT ACT ACT CTT CAG TCA GAT CAA GAG GAA ATT GAC TAT	6054
Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr	
1670 1675 1680	
GAT GAT ACC ATA TCA GTT GAA ATG AAG AAG GAA GAT TTT GAC ATT TAT	6102
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr	
1685 1690 1695	
GAT GAG GAT GAA AAT CAG AGC CCC CGC AGC TTT CAA AAG AAA ACA CGA	6150
Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg	
1700 1705 1710 1715	
CAC TAT TTT ATT GCT GCA GTG GAG AGG CTC TGG GAT TAT GGG ATG AGT	6198
His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser	
1720 1725 1730	

AGC TCC CCA CAT GTT CTA AGA AAC AGG GCT CAG AGT GGC AGT GTC CCT	6246
Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val Pro	
1735 1740 1745	
CAG TTC AAG AAA GTT GTT TTC CAG GAA TTT ACT GAT GGC TCC TTT ACT	6294
Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr	
1750 1755 1760	
CAG CCC TTA TAC CGT GGA GAA CTA AAT GAA CAT TTG GGA CTC CTG GGG	6342
Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly	
1765 1770 1775	
CCA TAT ATA AGA GCA GAA GTT GAA GAT AAT ATC ATG GTA ACT TTC AGA	6390
Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg	
1780 1785 1790 1795	
AAT CAG GCC TCT CGT CCC TAT TCC TTC TAT TCT AGC CTT ATT TCT TAT	6438
Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr	
1800 1805 1810	
GAG GAA GAT CAG AGG CAA GGA GCA GAA CCT AGA AAA AAC TTT GTC AAG	6486
Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys	
1815 1820 1825	
CCT AAT GAA ACC AAA ACT TAC TTT TGG AAA GTG CAA CAT CAT ATG GCA	6534
Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala	
1830 1835 1840	
CCC ACT AAA GAT GAG TTT GAC TGC AAA GCC TGG GCT TAT TTC TCT GAT	6582
Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp	
1845 1850 1855	
GTT GAC CTG GAA AAA GAT GTG CAC TCA GGC CTG ATT GGA CCC CTT CTG	6630
Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu	
1860 1865 1870 1875	
GTC TGC CAC ACT AAC ACA CTG AAC CCT GCT CAT GGG AGA CAA GTG ACA	6678
Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr	
1880 1885 1890	
GTA CAG GAA TTT GCT CTG TTT TTC ACC ATC TTT GAT GAG ACC AAA AGC	6726
Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser	
1895 1900 1905	
TGG TAC TTC ACT GAA AAT ATG GAA AGA AAC TGC AGG GCT CCC TGC AAT	6774
Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn	
1910 1915 1920	
ATC CAG ATG GAA GAT CCC ACT TTT AAA GAG AAT TAT CGC TTC CAT GCA	6822
Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala	
1925 1930 1935	
ATC AAT GGC TAC ATA ATG GAT ACA CTA CCT GGC TTA GTA ATG GCT CAG	6870
Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln	
1940 1945 1950 1955	

GAT	CAA	AGG	ATT	CGA	TGG	TAT	CTG	CTC	AGC	ATG	GGC	AGC	AAT	GAA	AAC	6918
Asp	Gln	Arg	Ile	Arg	Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	
				1960						1965					1970	
ATC	CAT	TCT	ATT	CAT	TTC	AGT	GGA	CAT	GTG	TTC	ACT	GTA	CGA	AAA	AAA	6966
Ile	His	Ser	Ile	His	Phe	Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	
				1975					1980					1985		
GAG	GAG	TAT	AAA	ATG	GCA	CTG	TAC	AAT	CTC	TAT	CCA	GGT	GTT	TTT	GAG	7014
Glu	Glu	Tyr	Lys	Met	Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	
				1990					1995				2000			
ACA	GTG	GAA	ATG	TTA	CCA	TCC	AAA	GCT	GGA	ATT	TGG	CGG	GTG	GAA	TGC	7062
Thr	Val	Glu	Met	Leu	Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	
								2010					2015			
CTT	ATT	GGC	GAG	CAT	CTA	CAT	GCT	GGG	ATG	AGC	ACA	CTT	TTT	CTG	GTG	7110
Leu	Ile	Gly	Glu	His	Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	
								2020							2035	
TAC	AGC	AAT	AAG	TGT	CAG	ACT	CCC	CTG	GGA	ATG	GCT	TCT	GGA	CAC	ATT	7158
Tyr	Ser	Asn	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	
								2040							2050	
AGA	GAT	TTT	CAG	ATT	ACA	GCT	TCA	GGA	CAA	TAT	GGA	CAG	TGG	GCC	CCA	7206
Arg	Asp	Phe	Gln	Ile	Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	
								2055						2065		
AAG	CTG	GCC	AGA	CTT	CAT	TAT	TCC	GGA	TCA	ATC	AAT	GCC	TGG	AGC	ACC	7254
Lys	Leu	Ala	Arg	Leu	His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	
								2070						2080		
AAG	GAG	CCC	TTT	TCT	TGG	ATC	AAG	GTG	GAT	CTG	TTG	GCA	CCA	ATG	ATT	7302
Lys	Glu	Pro	Phe	Ser	Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	
								2085					2095			
ATT	CAC	GGC	ATC	AAG	ACC	CAG	GGT	GCC	CGT	CAG	AAG	TTC	TCC	AGC	CTC	7350
Ile	His	Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	
								2100							2115	
TAC	ATC	TCT	CAG	TTT	ATC	ATC	ATG	TAT	AGT	CTT	GAT	GGG	AAG	AAG	TGG	7398
Tyr	Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	
								2120						2130		
CAG	ACT	TAT	CGA	GGA	AAT	TCC	ACT	GGA	ACC	TTA	ATG	GTC	TTC	TTT	GGC	7446
Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	
								2135						2145		
AAT	GTG	GAT	TCA	TCT	GGG	ATA	AAA	CAC	AAT	ATT	TTT	AAC	CCT	CCA	ATT	7494
Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	
								2150						2160		
ATT	GCT	CGA	TAC	ATC	CGT											

ACT CTT CGC ATG GAG TTG ATG GGC TGT GAT TTA AAT AGT TGC AGC ATG	7590
Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met	
2180 2185 2190 2195	
CCA TTG GGA ATG GAG AGT AAA GCA ATA TCA GAT GCA CAG ATT ACT GCT	7638
Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala	
2200 2205 2210	
TCA TCC TAC TTT ACC AAT ATG TTT GCC ACC TGG TCT CCT TCA AAA GCT	7686
Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala	
2215 2220 2225	
CGA CTT CAC CTC CAA GGG AGG AGT AAT GCC TGG AGA CCT CAG GTG AAT	7734
Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn	
2230 2235 2240	
AAT CCA AAA GAG TGG CTG CAA GTG GAC TTC CAG AAG ACA ATG AAA GTC	7782
Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val	
2245 2250 2255	
ACA GGA GTA ACT ACT CAG GGA GTA AAA TCT CTG CTT ACC AGC ATG TAT	7830
Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr	
2260 2265 2270 2275	
GTG AAG GAG TTC CTC ATC TCC AGC AGT CAA GAT GGC CAT CAG TGG ACT	7878
Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr	
2280 2285 2290	
CTC TTT TTT CAG AAT GGC AAA GTA AAG GTT TTT CAG GGA AAT CAA GAC	7926
Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp	
2295 2300 2305	
TCC TTC ACA CCT GTG GTG AAC TCT CTA GAC CCA CCG TTA CTG ACT CGC	7974
Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg	
2310 2315 2320	
TAC CTT CGA ATT CAC CCC CAG AGT TGG GTG CAC CAG ATT GCC CTG AGG	8022
Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg	
2325 2330 2335	
ATG GAG GTT CTG GGC TGC GAG GCA CAG GAC CTC TAC TGAGGGTGGC	8068
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr	
2340 2345 2350	
CACTGCAGCA CCTGCCACTG CCGTCACCTC TCCCTCCTCA GCTCCAGGGC AGTGTCCTC	8128
CCTGGCTTGC CTTCTACCTT TGTGCTAAAT CCTAGCAGAC ACTGCCTTGA AGCCTCCTGA	8188
ATTA ACTATC ATCAGTCCTG CATTTCTTTG GTGGGGGGCC AGGAGGGTGC ATCCAATTTA	8248
ACTTAACTCT TACCTATTTT CTGCAGCTGC TCCCAGATTA CTCCTTCCTT CCAATATAAC	8308
TAGGCAAAAA GAAGTGAGGA GAAACCTGCA TGAAAGCATT CTTCCCTGAA AAGTTAGGCC	8368
TCTCAGAGTC ACCACTTCCT CTGTTGTAGA AAAACTATGT GATGAACTT TGAAAAAGAT	8428
ATTTATGATG TTAAC TTGTT TATTGCAGCT TATAATGGTT ACAAATAAAG CAATAGCATC	8488

ACAAATTTC	CAAATAAAGC	ATTTTTTTCA	CTGCATTCTA	GTTGTGGTTT	GTCCAAACTC	8548
ATCAATGTAT	CTTATCATGT	CTGGATCCCC	GGGTGGCATC	CCTGTGACCC	CTCCCCAGTG	8608
CCTCTCCTGG	CCCTGGAAGT	TGCCACTCCA	GTGCCCACCA	GCCTTGTCTC	AATAAAATTA	8668
AGTTGCATCA	TTTTGTCTGA	CTAGGTGTCC	TTCTATAATA	TTATGGGGTG	GAGGGGGGTG	8728
GTATGGAGCA	AGGGGCAAGT	TGGGAAGACA	ACCTGTAGGG	CCTGCGGGGT	CTATTCGGGA	8788
ACCAAGCTGG	AGTGCAGTGG	CACAATCTTG	GCTCACTGCA	ATCTCCGCCT	CCTGGGTTCA	8848
AGCGATTCTC	CTGCCTCAGC	CTCCCGAGTT	GTTGGGATTC	CAGGCATGCA	TGACCAGGCT	8908
CAGCTAATTT	TTGTTTTTTT	GGTAGAGACG	GGGTTTCACC	ATATTGGCCA	GGCTGGTCTC	8968
CAACTCCTAA	TCTCAGGTGA	TCTACCCACC	TTGGCCTCCC	AAATTGCTGG	GATTACAGGC	9028
GTGAACCACT	GCTCCCTTCC	CTGTCTTCT	GATTTTAAAA	TAACTATACC	AGCAGGAGGA	9088
CGTCCAGACA	CAGCATAGGC	TACCTGCCAT	GCCCAACCGG	TGGGACATTT	GAGTTGCTTG	9148
CTTGGCACTG	TCCTCTCATG	CGTTGGGTCC	ACTCAGTAGA	TGCCTGTTGA	ATTCGTAATC	9208
ATGGTCATAG	CTGTTTCCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	ACAACATACG	9268
AGCCGGAAGC	ATAAAGTGTA	AAGCCTGGGG	TGCCTAATGA	GTGAGCTAAC	TCACATTAAT	9328
TGCGTTGCGC	TCACTGCCCC	CTTTCCAGTC	GGGAAACCTG	TCGTGCCAGC	TGCATTAATG	9388
AATCGGCCAA	CGCGCGGGGA	GAGGCGGTTT	GCGTATTGGG	CGCTCTTCCG	CTTCCTCGCT	9448
CACTGACTCG	CTGCGCTCGG	TCGTTTCGGCT	GCGGCGAGCG	GTATCAGCTC	ACTCAAAGGC	9508
GGTAATACGG	TTATCCACAG	AATCAGGGGA	TAACGCAGGA	AAGAACATGT	GAGCAAAAGG	9568
CCAGCAAAAG	GCCAGGAACC	GTAAAAAGGC	CGCGTTGCTG	GCGTTTTTCC	ATAGGCTCCG	9628
CCCCCCTGAC	GAGCATCACA	AAAATCGACG	CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	9688
ACTATAAAGA	TACCAGGCGT	TTCCCCCTGG	AAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	9748
CCTGCCGCTT	ACCGGATACC	TGTCCGCCTT	TCTCCCTTCG	GGAAGCGTGG	CGCTTTCTCA	9808
TAGCTCACGC	TGTAGGTATC	TCAGTTCGGT	GTAGGTCGTT	CGCTCCAAGC	TGGGCTGTGT	9868
GCACGAACCC	CCCGTTCAGC	CCGACCGCTG	CGCCTTATCC	GGTAACTATC	GTCTTGAGTC	9928
CAACCCGGTA	AGACACGACT	TATCGCCACT	GGCAGCAGCC	ACTGGTAACA	GGATTAGCAG	9988
AGCGAGGTAT	GTAGGCGGTG	CTACAGAGTT	CTTGAAGTGG	TGGCCTAACT	ACGGCTACAC	10048
TAGAAGGACA	GTATTTGGTA	TCTGCGCTCT	GCTGAAGCCA	GTTACCTTCG	GAAAAAGAGT	10108
TGGTAGCTCT	TGATCCGGCA	AACAAACCAC	CGCTGGTAGC	GGTGGTTTTT	TTGTTTGCAA	10168
GCAGCAGATT	ACGCGCAGAA	AAAAAGGATC	TCAAGAAGAT	CCTTTGATCT	TTTCTACGGG	10228

GTCTGACGCT CAGTGGAAACG AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA 10288
 AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATGAAGT TTTAAATCAA TCTAAAGTAT 10348
 ATATGAGTAA ACTTGGTCTG ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC 10408
 GATCTGTCTA TTTCGTTTAT CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT 10468
 ACGGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGCTCACC 10528
 GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC 10588
 TGCAACTTTA TCCGCCTCCA TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG 10648
 TTCGCCAGTT AATAGTTTGC GCAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTACAG 10708
 CTCGTGTTTT GGTATGGCTT CATTGAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG 10768
 ATCCCCCATG TTGTGCAAAA AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG 10828
 TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT 10888
 CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA 10948
 ATAGTGTATG CGGCGACCGA GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC 11008
 ACATAGCAGA ACTTTAAAAG TGCTCATCAT TGGAAAACGT TCTTCGGGGC GAAAACTCTC 11068
 AAGGATCTTA CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC 11128
 TTCAGCATCT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC 11188
 CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTTCA 11248
 ATATTATTGA AGCATTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT 11308
 TTAGAAAAAT AAACAAATAG GGGTTCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT 11368
 CTAAGAAACC ATTATTATCA TGACATTAAC CTATAAAAAT AGGCGTATCA CGAGGCCCTT 11428
 TCGTCTCGCG CGTTTCGGTG ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC 11488
 GGTCACAGCT TGTCTGTAAG CGGATGCCGG GAGCAGACAA GCCCGTCAGG GCGCGTCAGC 11548
 GGGTGTGGC GGGTGTGGG GCTGGCTTAA CTATGCGGCA TCAGAGCAGA TTGTACTGAG 11608
 AGTGCACCAT ATGCGGTGTG AAATACCGCA CAGATGCGTA AGGAGAAAAT ACCGCATCAG 11668
 GCGCCATTCG CCATTCAGGC TGCGCAACTG TTGGGAAGGG CGATCGGTGC GGGCCTCTTC 11728
 GCTATTACGC CAGCTGGCGA AAGGGGGATG TGCTGCAAGG CGATTAAAGTT GGGTAACGCC 11788
 AGGGTTTTCC CAGTCACGAC GTTGTA AAC GACGGCCAGT GCCAAGCTTG GGCTGCAG 11846

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTGAACCAA GAAGCTTCTC CCAGGTAAGT TGCTAATAAA GCTTGGCAAG AGTATTTCAA 60
GGAAGATGAA GTCATTAAGT ATGCAAAATG CTTCTCAGGC ACCTAGGAAA ATGAGGATGT 120
GAGGCATTTT TACCCACTTG GTACATAAAA TTATTGCTTT TCCTCTTCTT TTTTCTCCA 180
GAACCCACCA GTCTTGAAAC GCCATCAACG G 211

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTGGTATCC TTTTACAGC ACAACTTAAT GAGACAGATA GAACTGGTC TTGTAGAAAC 60
AGAGTAGTCG CTGCTTTTC TGCCAGGTGC TGAATTCTCT CCCCTGGGCT GTTTCATTT 120
TCTCAG 126

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTAAGTATCC TTTTACAGC ACAACTTAAT GAGACAGATA GAACTGGTC TTGTAGAAAC 60
AGAGTAGTCG CTGCTTTTC TGCCAGGTGC TGAATTCTCT CCCCTTCTCT TTTTCCTTT 120
TCTCAG 126

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCACCAUGG

10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGTTAATTT TAAAAAGCA GTCAAAAGTC CAAGTGGCCC TTGCGAGCAT TTACTCTCTC 60

TGTTTGCTCT GGTTAATAAT CTCAGGAGCA CAAACATTCC 100

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTTCTCTTT TCTTTTACAT GAAGGGTCTG GCAGCCAAAG CAATCACTCA AAGTTCAAAC 60

CTTATCATTT TTTGCTTTGT TCCTCTTGGC CTTGGTTTTG TACATCAGCT TTGAAAATAC 120

CATCCCAGGG TTAATGCTGG GGTAAATTTA TAACTAAGAG TGCTCTAGTT TTGCAATACA 180

GGACATGCTA TAAAAATGGA AAGATGTTGC TTTCTGAGAG ATA 223

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGAUCUCGAG AAAGCUAACA ACAAAGAACA ACAAACAACA AUCAGGAUAA CAAGAACGAA 60

ACAAUACAG CCACCAUGGA AAUAGAGCUC 90